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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/997,623

DATE: 04/12/2002

TIME: 14:24:36

Input Set : A:\0219us410-Mar2002-Sequence_Listing.txt

Output Set: N:\CRF3\04122002\I997623.raw

3 <110> APPLICANT: Maxygen Aps; Maxygen Holdings
5 <120> TITLE OF INVENTION: Protein C or activated protein C-like molecules
7 <130> FILE REFERENCE: 0219us410 - protein C
9 <140> CURRENT APPLICATION NUMBER: US 09/997,623
10 <141> CURRENT FILING DATE: 2001-11-29
12 <150> PRIOR APPLICATION NUMBER: US 09/978,917
13 <151> PRIOR FILING DATE: 2001-10-17
15 <160> NUMBER OF SEQ ID NOS: 48
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1383
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (1)..(1383)
28 <221> NAME/KEY: sig_peptide
29 <222> LOCATION: (1)...(126)
31 <221> NAME/KEY: mat_peptide
32 <222> LOCATION: (127)..(1383)
35 <400> SEQUENCE: 1
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37 Met Trp Gln Leu Thr Ser Leu Leu Leu Phe Val Ala Thr Trp Gly Ile
38 -40 -35 -30
40 tcc gcc aca cca gct cct ctt gac tca gtg ttc tcc agc agc gag cgt 96
41 Ser Gly Thr Pro Ala Pro Leu Asp Ser Val Phe Ser Ser Ser Glu Arg
42 -25 -20 -15
44 gcc cac cag gtg ctg cgg atc cgc aaa cgt gcc aac tcc ttc ctg gag 144
45 Ala His Gln Val Leu Arg Ile Arg Lys Arg Ala Asn Ser Phe Leu Glu
46 -10 -5 -1 1 5
48 gag ctc cgt cac agc agc ctg gag cgg gag tgc ata gag gag atc tgt 192
49 Glu Leu Arg His Ser Ser Leu Glu Arg Glu Cys Ile Glu Glu Ile Cys
50 10 15 20
52 gac ttc gag gag gcc aag gaa att ttc caa aat gtg gat gac aca ctg 240
53 Asp Phe Glu Glu Ala Lys Glu Ile Phe Gln Asn Val Asp Asp Thr Leu
54 25 30 35
56 gcc ttc tgg tcc aag cac gtc gac ggt gac cag tgc ttg gtc ttg ccc 288
57 Ala Phe Trp Ser Lys His Val Asp Gly Asp Gln Cys Leu Val Leu Pro
58 40 45 50
60 ttg gag cac ccg tgc gcc agc ctg tgc tgc ggg cac ggc acg tgc atc 336
61 Leu Glu His Pro Cys Ala Ser Leu Cys Cys Gly His Gly Thr Cys Ile
62 55 60 65 70
64 gac ggc atc ggc agc ttc agc tgc gac tgc cgc agc ggc tgg gag ggc 384

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65	Asp	Gly	Ile	Gly	Ser	Phe	Ser	Cys	Asp	Cys	Arg	Ser	Gly	Trp	Glu	Gly	
66					75					80					85		
68	cgc	ttc	tgc	cag	cgc	gag	gtg	agc	ttc	ctc	aat	tgc	tcg	ctg	gac	aac	432
69	Arg	Phe	Cys	Gln	Arg	Glu	Val	Ser	Phe	Leu	Asn	Cys	Ser	Leu	Asp	Asn	
70				90					95					100			
72	ggc	ggc	tgc	acg	cat	tac	tgc	cta	gag	gag	gtg	ggc	tgg	cgg	cgc	tgt	480
73	Gly	Gly	Cys	Thr	His	Tyr	Cys	Leu	Glu	Glu	Val	Gly	Trp	Arg	Arg	Cys	
74			105					110					115				
76	agc	tgt	gcg	cct	ggc	tac	aag	ctg	ggg	gac	gac	ctc	ctg	cag	tgt	cac	528
77	Ser	Cys	Ala	Pro	Gly	Tyr	Lys	Leu	Gly	Asp	Asp	Leu	Leu	Gln	Cys	His	
78		120					125					130					
80	ccc	gca	gtg	aag	ttc	cct	tgt	ggg	agg	ccc	tgg	aag	cgg	atg	gag	aag	576
81	Pro	Ala	Val	Lys	Phe	Pro	Cys	Gly	Arg	Pro	Trp	Lys	Arg	Met	Glu	Lys	
82	135					140					145				150		
84	aag	cgc	agt	cac	ctg	aaa	cga	gac	aca	gaa	gac	caa	gaa	gac	caa	gta	624
85	Lys	Arg	Ser	His	Leu	Lys	Arg	Asp	Thr	Glu	Asp	Gln	Glu	Asp	Gln	Val	
86				155					160					165			
88	gat	ccg	cgg	ctc	att	gat	ggg	aag	atg	acc	agg	cgg	gga	gac	agc	ccc	672
89	Asp	Pro	Arg	Leu	Ile	Asp	Gly	Lys	Met	Thr	Arg	Arg	Gly	Asp	Ser	Pro	
90			170					175					180				
92	tgg	cag	gtg	gtc	ctg	ctg	gac	tca	aag	aag	aag	ctg	gcc	tgc	ggg	gca	720
93	Trp	Gln	Val	Val	Leu	Leu	Asp	Ser	Lys	Lys	Lys	Leu	Ala	Cys	Gly	Ala	
94			185					190					195				
96	gtg	ctc	atc	cac	ccc	tcc	tgg	gtg	ctg	aca	gcg	gcc	cac	tgc	atg	gat	768
97	Val	Leu	Ile	His	Pro	Ser	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Met	Asp	
98		200					205					210					
100	gag	tcc	aag	aag	ctc	ctt	gtc	agg	ctt	gga	gag	tat	gac	ctg	cgg	cgc	816
101	Glu	Ser	Lys	Lys	Leu	Leu	Val	Arg	Leu	Gly	Glu	Tyr	Asp	Leu	Arg	Arg	
102	215					220				225					230		
104	tgg	gag	aag	tgg	gag	ctg	gac	ctg	gac	atc	aag	gag	gtc	ttc	gtc	cac	864
105	Trp	Glu	Lys	Trp	Glu	Leu	Asp	Leu	Asp	Ile	Lys	Glu	Val	Phe	Val	His	
106				235					240					245			
108	ccc	aac	tac	agc	aag	agc	acc	acc	gac	aat	gac	atc	gca	ctg	ctg	cac	912
109	Pro	Asn	Tyr	Ser	Lys	Ser	Thr	Thr	Asp	Asn	Asp	Ile	Ala	Leu	Leu	His	
110			250						255				260				
112	ctg	gcc	cag	ccc	gcc	acc	ctc	tcg	cag	acc	ata	gtg	ccc	atc	tgc	ctc	960
113	Leu	Ala	Gln	Pro	Ala	Thr	Leu	Ser	Gln	Thr	Ile	Val	Pro	Ile	Cys	Leu	
114			265					270					275				
116	ccg	gac	agc	ggc	ctt	gca	gag	cgc	gag	ctc	aat	cag	gcc	ggc	cag	gag	1008
117	Pro	Asp	Ser	Gly	Leu	Ala	Glu	Arg	Glu	Leu	Asn	Gln	Ala	Gly	Gln	Glu	
118		280					285					290					
120	acc	ctc	gtg	acg	ggc	tgg	ggc	tac	cac	agc	agc	cga	gag	aag	gag	gcc	1056
121	Thr	Leu	Val	Thr	Gly	Trp	Gly	Tyr	His	Ser	Ser	Arg	Glu	Lys	Glu	Ala	
122	295					300					305				310		
124	aag	aga	aac	cgc	acc	ttc	gtc	ctc	aac	ttc	atc	aag	att	ccc	gtg	gtc	1104
125	Lys	Arg	Asn	Arg	Thr	Phe	Val	Leu	Asn	Phe	Ile	Lys	Ile	Pro	Val	Val	
126				315					320					325			
128	ccg	cac	aat	gag	tgc	agc	gag	gtc	atg	agc	aac	atg	gtg	tct	gag	aac	1152
129	Pro	His	Asn	Glu	Cys	Ser	Glu	Val	Met	Ser	Asn	Met	Val	Ser	Glu	Asn	

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130          330          335          340
132 atg ctg tgt gcg ggc atc ctc ggg gac cgg cag gat gcc tgc gag ggc 1200
133 Met Leu Cys Ala Gly Ile Leu Gly Asp Arg Gln Asp Ala Cys Glu Gly
134          345          350          355
136 gac agt ggg ggg ccc atg gtc gcc tcc ttc cac ggc acc tgg ttc ctg 1248
137 Asp Ser Gly Gly Pro Met Val Ala Ser Phe His Gly Thr Trp Phe Leu
138          360          365          370
140 gtg ggc ctg gtg agc tgg ggt gag ggc tgt ggg ctc ctt cac aac tac 1296
141 Val Gly Leu Val Ser Trp Gly Glu Gly Cys Gly Leu Leu His Asn Tyr
142 375          380          385          390
144 ggc gtt tac acc aaa gtc agc cgc tac ctc gac tgg atc cat ggg cac 1344
145 Gly Val Tyr Thr Lys Val Ser Arg Tyr Leu Asp Trp Ile His Gly His
146          395          400          405
148 atc aga gac aag gaa gcc ccc cag aag agc tgg gca cct 1383
149 Ile Arg Asp Lys Glu Ala Pro Gln Lys Ser Trp Ala Pro
150          410          415
153 <210> SEQ ID NO: 2
154 <211> LENGTH: 461
155 <212> TYPE: PRT
156 <213> ORGANISM: Homo sapiens
158 <220> FEATURE:
159 <221> NAME/KEY: SIGNAL
160 <222> LOCATION: (1)...(42)
162 <221> NAME/KEY: CHAIN
163 <222> LOCATION: (43)...(461)
165 <400> SEQUENCE: 2
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167          -40          -35          -30
169 Ser Gly Thr Pro Ala Pro Leu Asp Ser Val Phe Ser Ser Ser Glu Arg
170          -25          -20          -15
172 Ala His Gln Val Leu Arg Ile Arg Lys Arg Ala Asn Ser Phe Leu Glu
173 -10          -5          -1 1 5
175 Glu Leu Arg His Ser Ser Leu Glu Arg Glu Cys Ile Glu Glu Ile Cys
176          10          15          20
178 Asp Phe Glu Glu Ala Lys Glu Ile Phe Gln Asn Val Asp Asp Thr Leu
179          25          30          35
181 Ala Phe Trp Ser Lys His Val Asp Gly Asp Gln Cys Leu Val Leu Pro
182          40          45          50
184 Leu Glu His Pro Cys Ala Ser Leu Cys Cys Gly His Gly Thr Cys Ile
185 55          60          65          70
187 Asp Gly Ile Gly Ser Phe Ser Cys Asp Cys Arg Ser Gly Trp Glu Gly
188          75          80          85
190 Arg Phe Cys Gln Arg Glu Val Ser Phe Leu Asn Cys Ser Leu Asp Asn
191          90          95          100
193 Gly Gly Cys Thr His Tyr Cys Leu Glu Glu Val Gly Trp Arg Arg Cys
194          105          110          115
196 Ser Cys Ala Pro Gly Tyr Lys Leu Gly Asp Asp Leu Leu Gln Cys His
197          120          125          130
199 Pro Ala Val Lys Phe Pro Cys Gly Arg Pro Trp Lys Arg Met Glu Lys

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200 135          140          145          150
202 Lys Arg Ser His Leu Lys Arg Asp Thr Glu Asp Gln Glu Asp Gln Val
203          155          160          165
205 Asp Pro Arg Leu Ile Asp Gly Lys Met Thr Arg Arg Gly Asp Ser Pro
206          170          175          180
208 Trp Gln Val Val Leu Leu Asp Ser Lys Lys Lys Leu Ala Cys Gly Ala
209          185          190          195
211 Val Leu Ile His Pro Ser Trp Val Leu Thr Ala Ala His Cys Met Asp
212          200          205          210
214 Glu Ser Lys Lys Leu Leu Val Arg Leu Gly Glu Tyr Asp Leu Arg Arg
215 215          220          225          230
217 Trp Glu Lys Trp Glu Leu Asp Leu Asp Ile Lys Glu Val Phe Val His
218          235          240          245
220 Pro Asn Tyr Ser Lys Ser Thr Thr Asp Asn Asp Ile Ala Leu Leu His
221          250          255          260
223 Leu Ala Gln Pro Ala Thr Leu Ser Gln Thr Ile Val Pro Ile Cys Leu
224          265          270          275
226 Pro Asp Ser Gly Leu Ala Glu Arg Glu Leu Asn Gln Ala Gly Gln Glu
227          280          285          290
229 Thr Leu Val Thr Gly Trp Gly Tyr His Ser Ser Arg Glu Lys Glu Ala
230 295          300          305          310
232 Lys Arg Asn Arg Thr Phe Val Leu Asn Phe Ile Lys Ile Pro Val Val
233          315          320          325
235 Pro His Asn Glu Cys Ser Glu Val Met Ser Asn Met Val Ser Glu Asn
236          330          335          340
238 Met Leu Cys Ala Gly Ile Leu Gly Asp Arg Gln Asp Ala Cys Glu Gly
239          345          350          355
241 Asp Ser Gly Gly Pro Met Val Ala Ser Phe His Gly Thr Trp Phe Leu
242          360          365          370
244 Val Gly Leu Val Ser Trp Gly Glu Gly Cys Gly Leu Leu His Asn Tyr
245 375          380          385          390
247 Gly Val Tyr Thr Lys Val Ser Arg Tyr Leu Asp Trp Ile His Gly His
248          395          400          405
250 Ile Arg Asp Lys Glu Ala Pro Gln Lys Ser Trp Ala Pro
251          410          415
255 <210> SEQ ID NO: 3
256 <211> LENGTH: 1257
257 <212> TYPE: DNA
258 <213> ORGANISM: Homo sapiens
260 <220> FEATURE:
261 <221> NAME/KEY: CDS
262 <222> LOCATION: (1)..(1257)
264 <400> SEQUENCE: 3
265 gcc aac tcc ttc ctg gag gag ctc cgt cac agc agc ctg gag cgg gag      48
266 Ala Asn Ser Phe Leu Glu Glu Leu Arg His Ser Ser Leu Glu Arg Glu
267 1          5          10          15
269 tgc ata gag gag atc tgt gac ttc gag gag gcc aag gaa att ttc caa      96
270 Cys Ile Glu Glu Ile Cys Asp Phe Glu Glu Ala Lys Glu Ile Phe Gln
271          20          25          30

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273 aat gtg gat gac aca ctg gcc ttc tgg tcc aag cac gtc gac ggt gac 144
274 Asn Val Asp Asp Thr Leu Ala Phe Trp Ser Lys His Val Asp Gly Asp
275      35      40      45
277 cag tgc ttg gtc ttg ccc ttg gag cac ccg tgc gcc agc ctg tgc tgc 192
278 Gln Cys Leu Val Leu Pro Leu Glu His Pro Cys Ala Ser Leu Cys Cys
279      50      55      60
281 ggg cac ggc acg tgc atc gac ggc atc ggc agc ttc agc tgc gac tgc 240
282 Gly His Gly Thr Cys Ile Asp Gly Ile Gly Ser Phe Ser Cys Asp Cys
283      65      70      75      80
285 cgc agc ggc tgg gag ggc cgc ttc tgc cag cgc gag gtg agc ttc ctc 288
286 Arg Ser Gly Trp Glu Gly Arg Phe Cys Gln Arg Glu Val Ser Phe Leu
287      85      90      95
289 aat tgc tcg ctg gac aac ggc ggc tgc acg cat tac tgc cta gag gag 336
290 Asn Cys Ser Leu Asp Asn Gly Gly Cys Thr His Tyr Cys Leu Glu Glu
291      100      105      110
293 gtg ggc tgg cgg cgc tgt agc tgt gcg cct ggc tac aag ctg ggg gac 384
294 Val Gly Trp Arg Arg Cys Ser Cys Ala Pro Gly Tyr Lys Leu Gly Asp
295      115      120      125
297 gac ctc ctg cag tgt cac ccc gca gtg aag ttc cct tgt ggg agg ccc 432
298 Asp Leu Leu Gln Cys His Pro Ala Val Lys Phe Pro Cys Gly Arg Pro
299      130      135      140
301 tgg aag cgg atg gag aag aag cgc agt cac ctg aaa cga gac aca gaa 480
302 Trp Lys Arg Met Glu Lys Lys Arg Ser His Leu Lys Arg Asp Thr Glu
303      145      150      155      160
305 gac caa gaa gac caa gta gat ccg cgg ctc att gat ggg aag atg acc 528
306 Asp Gln Glu Asp Gln Val Asp Pro Arg Leu Ile Asp Gly Lys Met Thr
307      165      170      175
309 agg cgg gga gac agc ccc tgg cag gtg gtc ctg ctg gac tca aag aag 576
310 Arg Arg Gly Asp Ser Pro Trp Gln Val Val Leu Leu Asp Ser Lys Lys
311      180      185      190
313 aag ctg gcc tgc ggg gca gtg ctc atc cac ccc tcc tgg gtg ctg aca 624
314 Lys Leu Ala Cys Gly Ala Val Leu Ile His Pro Ser Trp Val Leu Thr
315      195      200      205
317 gcg gcc cac tgc atg gat gag tcc aag aag ctc ctt gtc agg ctt gga 672
318 Ala Ala His Cys Met Asp Glu Ser Lys Lys Leu Leu Val Arg Leu Gly
319      210      215      220
321 gag tat gac ctg cgg cgc tgg gag aag tgg gag ctg gac ctg gac atc 720
322 Glu Tyr Asp Leu Arg Arg Trp Glu Lys Trp Glu Leu Asp Leu Asp Ile
323      225      230      235      240
325 aag gag gtc ttc gtc cac ccc aac tac agc aag agc acc acc gac aat 768
326 Lys Glu Val Phe Val His Pro Asn Tyr Ser Lys Ser Thr Thr Asp Asn
327      245      250      255
329 gac atc gca ctg ctg cac ctg gcc cag ccc gcc acc ctc tcg cag acc 816
330 Asp Ile Ala Leu Leu His Leu Ala Gln Pro Ala Thr Leu Ser Gln Thr
331      260      265      270
333 ata gtg ccc atc tgc ctc ccg gac agc ggc ctt gca gag cgc gag ctc 864
334 Ile Val Pro Ile Cys Leu Pro Asp Ser Gly Leu Ala Glu Arg Glu Leu
335      275      280      285
337 aat cag gcc ggc cag gag acc ctc gtg acg ggc tgg ggc tac cac agc 912

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